

EXHIBIT B

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>Thursday, April 28, 2005
>DNA92234 [Full]
>887 Sites [All Sites]
> [DNA92234], sheldens
> Lib309
>Sequence confirmed by phredphrap

          thal
          nlaIII  snaBI
          sphI  fndIII/mvnI
          nspHI  batUI  taiI
          taiI  nspI  bsh1236I
          maeII/hpyCH4IV bsiWI/epI  tsp509I [M.ecoRI-]
          aluI  hlnII/acyI cac8I  bsaAI  ecorI  t11I
          sapI  ahaII/bsaHI  mluI  rsaI  hpy188I  smII
          mboII  aatII  cac8I  aEIII  maeII/hpyCH4IV  paer7I
          bphI  sfcI  earI/ksp632I hpy99I hpyCH4V csp6I  aluI  apoI  avaI [M.taqI-]  mnlI  fnu4HI/bsaFI  hpy18
          1 TAGGTGACAC TATAGAGAG CTATGACGC GCATGCACGC GTACGTAAGC TCGGAATTGC GCTCGAGGGA TGAATACCTC CGAGCCGCT TTGTTCTCCA
            ATCCACTGTG ATATCTTCTC GATACTGCAG CGTAGCTGCG CATGCATTGC AGCCTTAAGC CGAGCTCCTT ACTTATGGAG GCTTCGCGCA AACAGAGGT
            ^insert starts here

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Gseqgdit, DNA92234 [Full], page 1

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scrFI[M.hpaII-]
ncII
mspI
hpaII
dsaV
bspAI bssKI bsp1286
bbsI bslI bsmFI tail bmyI
aluI mnlI mboII bsaJI maeII/hpyCH4IV
101 GATGTGATA GCTCCACTAT ACCAGCCTCG TCTTCCCTCC GGGGACACAC GTGGGTACAG GCACAGAGAG ATATTATATG TCACCCCTCTT GGGGCTTTCA
CTACACTTAT CGAGGTGATA TGGTCGGAGC AGRAGGAGG CCCCCTGTG CACCCAGTCC CGTGTCTCTC TATATAATTAC AGTGGAGCA CCCCAGAAAGT
sau3AI
mboI/ndelI[dam-]
dpmI[dam-]
dpmI[dam+]
alwI[dam-]
nlaIV
bstXI/xhoII
bamHI bslI
hpy188I bstXI alwI[dam-] hpy188III
bfaI eco57I bpmI/gsuI[dcn-] bslI avai
201 TGGGACTCCC TCTGCCACAT TTTTGGAGG TTGGGAAGT TGCTAGAGGC TTCAGACTC CAGCCTAATG GATCCCAAC TCGGAGAAAT GGCTGGCTCC
ACCTGAGGG AGACGGGTGA AAAACCTCC AACCTTTCA AGCATCTCC AGTCTTGAG GTGGATTAC CTAGGTTTG AGCCTCTTA CCGACGCAGG
M D P K L G R M A A S
^MET

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Gseqedit, DNA92234 [Full], page 2

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fnu4HI/bsoFI
tseI acI
tseI mwoI thal nlaIII haeII
mwoI fnu4HI/bsoFI nspHI mspI
fnu4HI/bsoFI fnuDII/mvnI scrFI[M.hpaII-]
bbvI bbvI bstUI(M.hhaI-) ncII
tseI tseI bsh1236I dsav hinPI bpuAI mba
mwoI fnu4HI/bsoFI hinPI nspI hphi mwoI hpaII bbsI: rsaI mnlI
fnu4HI/bsoFI hhaI/cfoI mnlI acII bssKI xmiI mboII csp6I econI
cac8I bbvI bbvI bpmI/gsuI(dcm-) bseRI mnlI bslI bsaJI hhaI/cfoI asp700 bseRI bslI
301 CTGCTGGCTG TGCTGCTGCT GCTGCTGGAG CGCGGCATG TCTCTGACC CTCCCGCCC CCGGCGCTGT TAGAGAAAGT CTTCCAGTAC ATTGACCTCC
GACGACCGAC ACGACGACGA CGACGACCTC GCGCCGTACA AGAGGAGTGG GAGGGGCGGG GCGCGCGACA ATCTCTTTCA GAAGGTGATG TAACTGGAGG
12 L L A V L L L L L E R G M F S S P S P P A L L E K V F Q Y I D L H

mboII
earI/ksp632I
sapI
alul
setI
sacI
hgaI/aspHI(M.aluI-
ec1136II
bsp1286(M.aluI-)
bsiHKA I hpy188I
hpy188I bmyI eco57I ea
mnlI eco57I banII(M.aluI-) cf
tth111I/aspI
pleI
pflFI
mlyI
hinFI
haeIII/palI pflFI
mscI/balI mlyI
eaeI taqI hinFI
cfrI hpy188III
apoI alwNI(dcm-) haeIII/palI pflFI
foxi tsp509I alw26I/bsmAI mscI/balI mlyI
bstF5I hpyCH4V eaeI taqI hinFI
hpy188III bsgI hgaI eco57I mnlI eco57I banII(M.aluI-) ea
401 ATCAGGATGA ATTTGTGCAG ACGCTGAGG AGTGGGTGCC CATCGAGAGC GACTCTGTCC AGCCTGTGCC TCGCTTCAGA CAAGAGCTCT TCAGAAATGAT
TAGTCCTACT TAAACAGGTC TCGGACTTCC TCACCCACCG GTAGCTCTCG CTGAGACAGG TCGGACACGG AGCGAAGTCT GTTCTCGAGA AGTCTTACTA
46 Q D E F V Q T L K E W V A I E S D S V Q P V P R F R Q E L F R M M
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GseqEdit, DNA92234 [Full], page 3

mwol
scrFI[dcn-]
pspGI sau96I[M.haeIII-]
mvaI pspOMI/bsp120I
ecORI[dcn-]
dsav[dcn-]
bstNI nlaIV
bsaKI[dcn-]
hinPI bsp1286[M.haeIII-]
hhaI/cfoI sfiI
tseI bsaJI bmyI
fnu4HI/bsoFI sau96I[M.haeIII-]
bbvI apyI[dcn+]
hpyCH4V banII[M.haeIII-]
sfci haeII apaI mnlI
tseI acII tseI alwNI[dcn-] haeIII/palI bsaJI
mwol fnu4HI/bsoFI pstI[M.HI-] nlaIV haeIII/palI
bceAI bbvI fnu4HI/bsoFI ecoO109I/draII
haeIII/palI bbvI alw26I/bmaI bgli[M.haeIII-] pshAI avaII alw26I/bmaI mnlI
501 GCCCGTGGCT CCGGACACGC TGCAGCGGCT GGGGGCCCT GTGGCTCGG TGGACATGGG TCCTCAGCAG CTGCCCCGATG GTCAGAGTCT TCCATATACCT
CCGGCACCGA CGCCTGTGGC AGTCTGTGGC CCCCCGGGCA CACCGGAGCC ACCTGTACCC AGGAGTCGTC GACGGGCTAC CAGTCTCAGA AGTTATGGA
79. A V A A D T L Q R L G A R V A S V D M G P Q Q L P D G Q S L P I P

GSeqEdit, DNA92234 [Full], page 4

```

eaeI[dcn-]
scrFI[dcn-]
pdpGI
mval
ecorII[dcn-]
dsav[dcn-]
bstNI bslI
bssXI[dcn-]
apyI[dcn+]
fokI cfrI bsrI
bstFSI haeIII/palI
601 CCCGTCATCC TGGCCGAAC T GGGAGCGAT CCCACGAAAG GCACCGTGTG CTTCTACGGC CACTTGGAGC TGCAGCCTGC TGACCGGGGC GATGGGFGGC
GGGCAGTAGG ACCGGCTTGA CCCTCGCTA GGGTGTTC CGTGGCACAC GAAGATGCCG GTGAACCTGC ACCTGGGACG ACTGGCCCCG CTACCCACCG
112 P V I L A E L G S D P T K G T V C F Y G H L D V Q P A D R G D G W L

scrFI[M.hpaII-]
ncII
tseI
fnu4HI/bsoFI mspI
hpaII
dsav
bssKI
bsaJI
maeII/hpyCH4IV
btrI hpyCH4V
601 CCCGTCATCC TGGCCGAAC T GGGAGCGAT CCCACGAAAG GCACCGTGTG CTTCTACGGC CACTTGGAGC TGCAGCCTGC TGACCGGGGC GATGGGFGGC
GGGCAGTAGG ACCGGCTTGA CCCTCGCTA GGGTGTTC CGTGGCACAC GAAGATGCCG GTGAACCTGC ACCTGGGACG ACTGGCCCCG CTACCCACCG
112 P V I L A E L G S D P T K G T V C F Y G H L D V Q P A D R G D G W L

sau3AI mwoI
bslI
sau96I[M.haeIII-] dpnII[dam-] hi
hh
haeIII/palI
alwI[dam-] hae
ecc0109I/draII
601 CCCGTCATCC TGGCCGAAC T GGGAGCGAT CCCACGAAAG GCACCGTGTG CTTCTACGGC CACTTGGAGC TGCAGCCTGC TGACCGGGGC GATGGGFGGC
GGGCAGTAGG ACCGGCTTGA CCCTCGCTA GGGTGTTC CGTGGCACAC GAAGATGCCG GTGAACCTGC ACCTGGGACG ACTGGCCCCG CTACCCACCG
112 P V I L A E L G S D P T K G T V C F Y G H L D V Q P A D R G D G W L

sau96I
nlaiV
avaII
accI
mnlI
mnlI mcrI
bsrI bslEI
601 CCCGTCATCC TGGCCGAAC T GGGAGCGAT CCCACGAAAG GCACCGTGTG CTTCTACGGC CACTTGGAGC TGCAGCCTGC TGACCGGGGC GATGGGFGGC
GGGCAGTAGG ACCGGCTTGA CCCTCGCTA GGGTGTTC CGTGGCACAC GAAGATGCCG GTGAACCTGC ACCTGGGACG ACTGGCCCCG CTACCCACCG
112 P V I L A E L G S D P T K G T V C F Y G H L D V Q P A D R G D G W L
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scrFI[dcm-]      mnlI
pspGI            bpmI/gsuI[dcm-]
mvaI             scrFI[dcm-]
ecoreI[dcm-]     pspGI
dsaV[dcm-]       mvaI
bstNI            ecorII[dcm-]
bsp1286          dsaV[dcm-]
bmyI bssKI[dcm-] bstNI
hpy188I apyI[dcm+] dpnII[dcm-]
eco57I bsaJI    bsp1286
mwoI banII bpmI/gsuI[dcm-] bsp1286
801 CGCCTTCAGA GCCCTGGAGC AAGATCTTCC TGTGATATAC ATATTCATCA TTGAGGGGAT GGAAGAGGCT GGCTCTGTG CCCCTGGAGGA ACTTGTGGAA
    GCGGAAGTCT CGGACCTCG TTCTAGAAGG ACACTTATAG TTAAAGTAGT AACTCCCTTA CCTTCTCGA CCGAACHAC GGGACCTCCT TGAACACCTT
179 A E R A L E Q D L P V N I K F I I E G M E E A G S V A L E E L V E
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GSeqEdit, DNA92234 [Full], page 6

```

scrFI{
ncII
mspI
hpaII
dsvV
bssKI
bsaJI
xnaI/ps
smaI
scrFI[M
ncII
dsav
bssKI
bsaJI
avaI[M.
nlaIV
sau3AI
mboI/ndeII(dam-)
dpnII(dam-)
dpnI(dam+)
alwI(dam-)
cac8I
tflI
sau96I mboII
avaII hinfI
901 AAAGRAAGG ACCGATTCCT CTCTGGTGTG GACTACATNG TAATTTCAGA TAACCTGTGG ATCAGCCAAA GGAAGCCAGC AATCACTTAT GGAACCCGGG
TTTCTTTTCC TGGCTAAGAA GAGACCCACAC CTGATGTARC ATTAAGTCT ATTGACACC TAGTCGGTTT CCTTCGGTCG TTAGTGATA CCTTGGGCC
212 K E K D R F F S G V D Y I V I S D N L W I S Q R K P A I T Y G T R G

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GSeqEdit, DNA92234 [Full], page 7

GGseqEdit, DNA92234 [Full], page 8

```
scrFI[dcm-]
pspGI
mvaI
ecorII[dcm-]
dsaV[dcm-]
bstNI
bssKI[dcm-]
sau96I[dcm-]
nlaIV
avaII[dcm-]
scrFI[dcm-]
pspGI apyI[dcm+]
mvaI bsmFI
ecorII[dcm-]
dsaV[dcm-]
bstNI bsaJI
bssKI[dcm-] tfII
apyI[dcm+] hinfI
mboII
1101 TCTTCTCGGT AGCCTGCTAG ACTCGTCTGG TCATATCCFG GTCCCTGGAA TCTATGATGA AGTGGTTCCT CTTACAGAAG AGGRANTAA TACATACAAA
AGAGAGGCCA TCGGACCATC TGAGCAGACC AGTATAGGAC CAGGACCTT AGATACTACT TCACCAAGGA GAATGCTTC TCCTTTATTT ATGTATGTTT
279 L L G S L V D S S G H I L V P G I Y D E V V P L T E E E I N T Y K
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GSeqEdit, DNA92234 [Full], page 9

```

rsal
csp6I
nlaIV
kpnI
banI
asp718
bpmI/gsuI{dcm}
hpy188III
acc65I
mnII
hpyCH4V
mnII
hpy188III
mnII
tfII
mnII
bseRI
hinfI
hpyCH4V
mnII
1201 GCCATCCATC TAGACCTAGA AGAATACCGG AATAGCAGCC GGGTTGAGAA ATTCTGTTT GATACCTAAGG AGGCGATTCT AATGCACCTC TGGAGGTACC
CGGTAGGTAG ATCTGGATCT TCTTATGGCC TTATCGTCGG CCCAACTCTT TAAAGACAAG CTATGATTC CCTCTAAGA TTACGTGGAG ACCTCCATGG
312 A I H L D L E E Y R N S S R V B X F L F D T K E E I L M H L W R Y P

haeIII/palI
eaeI{dcm-}
cfrI
scrFI{dcm-}
pspGI
mvaI
ecorII{dcm-}
dsav{dcm-}
bstNI
bssKI{dcm-}
apyI{dcm+}
xmnI
asp700
bsm
rmaI
maeI
bfaI
tsp509I
apoI
xmnI
asp700
bsm
rmaI
maeI
bfaI
1301 CATCTCTTTC TATTCATGGG ATCGAGGGCG CGTTTGATGA GCCTGGAACT AAAACAGTCA TACCTGGCCG AGTTATAGGA AAATTTTCAA TCCGTCTAGT
GTAGAGAAAG ATAAGTACCC TAGCTCCCGC GCRAACTACT CGGACCTTGA TTTTGTCACT ATGGACCGGC TCATATCCT TTTRAAGTT AGCAGATCA
346 S L S I H G I E G A F D E P G T K T V I P G R V I G K F S I R L V

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GSeqEdit, DNA92234 [Full], page 10

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pl      nlaiII      tsp45I      mboI      bstXI      nlaiII
ml      mslI      maeIII      hphI      hpy188III      asp700      bstXI
hi      xmnI      mboI      hpy188III      asp700      bstXI
nlaiII      nlaiII
1401 CCTTCACATG AATGTGCTCG CGGTGGGAAA ACAGGTGACA CGACATCTTG AGATGTGTT CTCCTAAAAGA AATAGTCCCA ACAAGATGGT TGTTCCTCAG
GGAGGTGTAC TTACACAGAC GCCACCTTTT TGTCCACTGT GCTGTAGAC TTCTACACAA GAGGTTTCT TTATCAAGGT TGTTCCTACCA ACAAGGTAC
379 P H M N V S A V E K Q V T R H L E D V F S K R N S S N K M V V S M

tspRI
sau      hpy188I
mbo      sau3AI bst4CI/hpyCH4III
dpm      mboI/ndeII[dam-]
dpm      fnu4HI/bsoFI dpmII[dam-]
alw      bbsI      bbsI      dpmI[dam+]
1501 ACTCTAGGAC TACACCCGTG GATTGCAAT ATTGATGACA CCCAGTATCT CGCAGCAAAA AGAGCGATCA GAACAGTGT TGGACACGAA CCAGATATGA
TGGATCCTCG NTGTGGGCAC CTAACGTTTA TAACTACTGT GGGTCATAGA GCGTCGTTT TCTGGCTAGT CTGTGACAA ACCTTGCTT GGTCTATACT
412 T L G L H P W I A N I D D T Q Y L A A K R A I R T V F G T E P D M I
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GSeqEdit, DNA92234 [Full], page 11

```
sau3AI
mboI/ndeII[dam-]
dpmII[dam-]
fokI dpmI[dam+]
bstF5I
scrFI[M.hpaII-]
ncII alwI[dam-]
mspI nlaIV
hpaII bstYI/xhoII
dsaV bamHI
bstKI alwI[dam-] mspI/mfeI
tsp509I mspI/mfeI
1601 TCCGGGATGG ATCCACCATT CCAATTCCTA AATGTTCCA GGAGATCCTC CACAAGAGCG TGGTGCTAAT TCCGCTGGGA GCTGTTGATG ATGGAGAACA
AGGCCCTACC TAGTGGTAA GGTAAACGGT TTTACAGGT CCTCTAGCAG GTGTTCTCGC ACCACGATTA AGGCGACCCCT CGACAACTAC TACCTCTTGT
446 R D G S T I P I A K M F Q E I V H K S V V L I P L G A V D D G E H

sau3AI
scrFI[dcn-]
pspGI mboI/ndeII[dam-]
mvaI dpmII[dam-]
ecoRII[dcn-]
dsaV[dcn-]
bstNI dpmI[dam+]
bstKI[dcn-]
tsp509I mspAII/nspBII
apVI[dcn+] mvoI acII aluI
1701 TTCCGAGAAAT GAGAAATCA ACAGGTGGA CFACATAGAG GGAACCAAT TATTGCTGC CTTTCTTA GAGATGGCC AGCTCCATTA ATCACAAGAA
AAGGCTCTTA CTCCTTTAGT TGTCACCTT GATGATCTC CCTTGGTTTA ATAAACGACG GAAAAGAAAT CTCTACCGG TOGAGGTAAT TAGTGTCTT
479 S Q N E K I N R W N Y I E G T K L F A A F F L E M A Q L H O

tru9I
tseI
nlaIV. fnu4HI/bsoFI
mnlI tsp509I bboVI ddeI
sau96I[M.haeIII-]
haeIII/palI aseI/asnI/vspI
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GSeqEdit, DNA92234 [Full], page 12

```
sau3AI
mboI/ndeII[dam-]
dpmII[dam-]
dpmI[dam+]
hpy188I
sau3AI tspRI
hpy188I alwI[dam-]
rmaI mboI/ndeII[dam-] hphI
maeI dpmII[dam-] tfir mnlI foki bfaI foki bfaI
bfaI dpmI[dam+] hinfI[M.hphI-] bstF3I bstF5I hpy188III
1801 CCTTCTAGTC TGATCTGATC CACTGACAGA TTCACCTCC CCACATCCCT AGACAGGGAT GGAATGTAAA TATCCAGAGA ATTTGGGTCT AGTATAGTAC
GGAAGATCAG ACTAGACTAG GTGACTGTCT AAGTGGAGG GGTGTAGGA TCTGTCCCTA CCTTACATTT ATAGGTCTCT TAACCCAGA TCATATCATG
sau96I
nlaIV
avaII hpyCH4V
ppuMI bsgI
ecoO109I/draII
tru9I tspRI
mseI bamFI btsI
ahaII/draI ecoRV alwI[dam-] sspI
1901 ATTTTCCCTT CCATTTAAA TGCTTGGGA TATCTGGATC AGTAAATAAA TATTCAAG GCACAGATGT TGAATAGGT TTAAAGGTCC CCACGTGCACA
TAAAGGGAA GGTAATTTT ACAGAACCTT ATAGACCTAG TCATTATTTT ATAAAGTTT CGTGTCTACA ACCTTACCA ARTTCCAGG GGTGACGTGT
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GSeqEdit, DNA92234 [Full], page 13

[illegible]

```
scrFI[M.hpaII-]
ncII
mspI
hpaII
dsav
bssKI          sau96I rsal
xmaI/pspAI     rsrII/cspI
smaI           nroI   nlaIV
scrFI[M.hpaII-] cpoI   kpaI   hpyCH4V
acII
fnu4HI/bsaFI   taqI   nciI   hpy188III csp6I
haeIII/palI    sstI   salI   dsav   bspMI   bani   sfcI
mcrI           sacI   hincII/hindII[M.taqI-] avall[M.hpaII-]
eagI/xmaIII/eclXI aluI accI[M.taqI-] tru9I mspI   asp718
eaeI           hgiAI/aspHI[M.aluI-] mseI bspEI cfr10I/bsrFI
cfrI           kmaI   ecl136II   bssKI   aseI/asnI/vspI   acc65I   cac8I
bslEI          maeI   bsp1286[M.aluI-] xmiI   tsp509I   bsaWI   pstI
notI           bfaI   bslHKAI   bsaJI   tsp509I   bsaWI   ageI   sse8387I
fnu4HI/bsaFI   bmyI   hpy99I   avall[M.hpaII-] hpaII mspI bspMI   rsal
acII           speI   banII[M.aluI-]   asp700   accIII hpaII sbfI   csp6I aluI   sf
2301 AAAAAAATAA AAAGGGCGGC CGCCGACTAG TGAGCTCGTC GACCCGGGAA TTAATTCGG ACGGCTACCT GCAGGCGTAC CAGCTTTCCC
TTTTTTTTTT TTTTTTTTTT TTTCCCGCCG GCGGCTGATC ACTCGAGCAG CTGGCCCTT AATTAAGGCC TGGCCATGGA CGTCCGCATG GTCGAARGGG
```

```
pleI
mlyI
hinfI      aluI
2401 TATAGTGAAGT CGTATTAGAG CTTGG
ATATCACTCA GCATAATCTC GAACC
```


> length: 2425

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aatII (GACGTC) :
acc65I (GGTACC) :
accI (GTMKAC) :
accIII (TCCGGA) :
acII (CCGC) :
acyI (GRCGYC) :
afIIII (ACRYGT) :
ageI (ACCGGT) :
ahaII (GRCGYC) :
ahaIII (TTTAAA) :
alul (AGCT) :
alw26I (CAGNNCTG) :
alwI (GGATCNNN) :
alwNI (CAGNNCTG) :
apaI (GGGCCC) :
apoI (RAATTY) :
apyl (CCWGG) :
asoI (ATTAAT) :
asnI (ATTAAT) :
asp700 (GAANNNTTC) :
asp718 (GGTACC) :
aspHI (GWGCWC) :
aspI (GACNNNGTC) :
avaI (CYCGRG) :
avaII (GGWCC) :
balI (TGGCCA) :
bamHI (GGATCC) :
banI (GGYRCC) :

25
1295 2374
727 1117 2348
2366
86 332 355 511 1420 1672 2326 2330
25
37
2371
25
1914
19 48 110 485 569 1006 1680 1781 2016 2343 2392 2419
418 523 565
270 271 628 785 959 1319 1599 1609 1610 1817 1936
418 523 565
533
54 409 841 1249 1381 1879
528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
1787 2219 2360
1787 2219 2360
375 1159 1379 1469 2358
1295 2374
484 2152 2342
451
62 280 995 2353
559 705 909 1140 1985 2143 2369
437
270 1609
640 1295 2374
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banII (GRCGYC): 484 533 809 2342
bbsI (GAAGACNNNNNN): 130 379 587
bbvI (GCAGC): 292 312 315 318 321 508 519 522 567 570 672 1235 1552 1756 2017 2024
bceAI (ACGGCNNNNNNNNNN): 502 656
bfeI (CTAG): 243 1210 1216 1396 1504 1805 1849 1889 2140 2337
bglI (GCCNNNNNGGC): 535
bglII (AGATCT): 822
bmyI (GDGCHC): 159 484 533 809 2152 2342
bpmI (CTGGAG): 96 258 325 814 883 1290
bpuAI (GAAGACNNNNNNNN): 130 379 587
bsaAI (YACGTR): 42
bsaHI (GRCGYC): 25
bsaI (GGTCTCNNNNNN): 1034 2234
bsaJI (CCNNGG): 139 359 503 528 545 684 812 881 995 996 1143 1516 2060 2353
bsaWI (WCCGGW): 1226 2127 2366 2371
bserI (GAGGAGNNNNNNNNNN): 342 749 1270
bsgI (GTGCAG): 415 670 1994
bsh1236I (CGCG): 38 331 1329
bslEI (CGRYCG): 755 2327
bslHKAI (GWGCWC): 484 2152 2342
bslWI (CGTACG): 40
bslI (CCNNNNNNNGG): 135 184 274 275 354 396 614 631 771 1847 1848 2060
bsmAI (GTCTC): 1034 2235
bsmAI (GTCTC): 1034 2235
bsmFI (GGGACNNNNNNNNNNNN): 143 202 297 1141 1399 1986
bsoFI (GCNGC): 85 292 312 315 318 321 332 508 519 522 567 570 672 1235 1552 1756
bsp120I (GGGCCC): 2017 2024 2326 2329
bsp1286I (GDGCHC): 533
bspCNI (CTCAGNNNNNNNNNN): 159 484 533 809 2152 2342
563 1050
GSeqEdit, DNA92234 [Full], page 17

bspEI (TCCGGA) : 2366
bspHI (TCATGA) : 1074
bspMI (ACCTGC) : 2377
bspMYI (TCCGGA) : 2366
bsrFI (RCCGGY) : 2371
384 618 1542
bsrI (ACTGGN) : 139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342
bsgKI (CCNGG) : 1363 1602 1638 2061 2353 2354
2155
bsSSI (CTCGTG) : 643 1354 1573
bst4CI (ACNGT) : 641
bstAPI (GCANNNNNTGC) : 503 1516
bstDSI (CCRYGG) : 405 606 857 1068 1203 1605 1844 1857 2175
bstFSI (GGATG) : 528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
bstNI (CCWGG) : 38 331 1329
bstUI (CGCG) : 260 1478
bstXI (CCANNNNNTGG) : 270 822 1609
bstYI (RGATCY) : 503 1516
btgI (CCRYGG) : 667
btrI (CACGTC) : 1992
btsI (GCAGTGN) : 31 35 303 675 868 975 2020 2381
cac8I (GCNNGC) : 330 364 525 800 1328
cfoI (CGGC) : 2371
cfr10I (RCCGGY) : 437 500 611 657 1365 2327
cfrI (YGGCCR) : 2368
cplI (CGGWCCG) : 41 387 1296 1897 2375 2387
csp6I (GTAC) : 2368
cspI (CGGWCCG) : 563 1050 1265 1767
ddeI (CTNAG) : 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
dpnI (GATC) : 2183

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dpnII (GATC) : 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
2183
draI (TTTAAA) : 1914
draII (RGGNCCY) : 532 558 768 1984 2142
642
draIII (CACNNNGTG) : 503 1516
dsaI (CCRYGG) : 139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342
dsaV (CCNGG) : 1363 1602 1638 2061 2353 2354
437 500 611 657 1365 2327
eaeI (YGGCCR) : 2327
eagI (CGGCCG) : 15 487 862 1100 1177
earI (CTCTTCNNNN) : 484 2342
ecI136II (GAGCTC) : 2327
ecLXI (CGGCCG) : 250 424 474 489 804
eco57I (CTGAAG) : 396
ecoNI (CCTNNNNNAGG) : 532 558 768 1984 2142
ecoO109I (RGGNCCY) : 54
ecoRI (GAATTC) : 528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
ecoRII (CCWGG) : 1929
ecoRV (GATATC) : 85 292 312 315 318 321 332 508 519 522 567 570 672 1235 1552 1756
fnu4HI (GCNGC) : 2017 2024 2326 2329
38 331 1329
fnuDII (CGCG) : 405 606 857 1068 1203 1605 1844 1857 2175
fokI (GGATG) : 96 258 325 814 883 1290
gsuI (CTGGAG) : 363 524 799
haeII (RGGCGY) : 438 501 534 543 612 658 769 1366 1776 2328
haeIII (GGCC) : 295 420
hgaI (GACGC) : 484 2152 2342
hglAI (GAGGWC) : 330 364 525 800 1328
hhaI (GGCC) : 330 364 525 800 1328
hinPI (GGCC) :
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hincII (GTYRAC): 2348
hindII (GTYRAC): 2348
hinfI (GATC): 204 451 585 914 1120 1148 1275 1500 1829 2070 2407
hlnI (GRCGYC): 25
hpaII (CCGG): 139 361 584 996 1227 1239 1602 2128 2354 2367 2372
hphI (GGTGA): 3 181 346 1023 1434 1832
hpy188I (TCNGA): 51 79 252 476 491 582 806 946 1568 1809 1814
hpy188III (TCNNGA): 97 281 402 443 1051 1074 1209 1289 1446 1873 1933 2156 2366
hpy99I (CGWCG): 27 2347
hpyCH4III (ACNGT): 643 1354 1573
hpyCH4IV (ACGT): 26 43 149 668
hpyCH4V (TGCA): 34 416 521 671 1030 1283 1524 1995 2023 2051 2104 2380
kpnI (GATACC): 1295 2374
ksp632I (CTCTTCNNNN): 15 487 862 1100 1177
maeI (CTAG): 243 1210 1216 1396 1504 1805 1849 1889 2140 2337
maeII (ACGT): 26 43 149 668
maeIII (GTNAC): 4 180 1435 2158
mboI (GATC): 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
2183
mboII (GAAGA): 15 131 380 488 588 825 862 917 1101 1177 1219 1450
mclI (CGRYCG): 755 2327
mfeI (CAATTG): 1622
mluI (ACGGGT): 37
mlyI (GAGTCNNNN): 204 451 585 1120 1500 2407
mnlI (CCTC): 65 77 126 185 209 227 246 344 350 396 469 545 562 598 724 749 853
865 886 1021 1168 1180 1270 1287 1293 1324 1402 1738 1835 2005 2146
2366
mroI (TCCGGA): 437
mscI (TGGCCA): 175 1788 1915 1981 2220 2361
mseI (TTAA): 400 1405 1407
mslI (CAYNNNRRTG): GSeqEdit, DNA92234 [Full], page 20

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mspAI(CMGCKG):
mspI(CCGG):
munI(CAATTG):
mvaI(CCWGG):
mvtI(CGCG):
mwvI(GCNRNNNNNGC):
ncII(CCSGG):
ndeII(GATC):

nlaIII(CATG):
nlaIV(GGNCC):
notI(GCGGCCGC):
napBI(CMGCKG):
nspHI(RCATGY):
nspI(RCATGY):
paerYI(CTCGAG):
pall(GGCC):
pf1FI(GACNNNGTC):
pleI(GAGTCNNNN):
ppuMI(RGGWCCY):
pshAI(GACNNNGTC):
pspAI(CCCGGG):
pspGI(CCWGG):
pspOMI(GGGCCC):
pstI(CTGCAG):
pvuII(CAGCTG):
rcaI(TCATGA):
rmaI(CTAG):
rsaI(GTAC):
rseII(CGGWCCG):

568 1672
139 361 684 996 1227 1239 1602 2128 2354 2367 2372
1622
528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
38 331 1329
303 312 315 321 357 502 535 641 650 793 802 1555 1665
139 360 684 995 996 1239 1602 2353 2354
271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
2183
32 199 336 555 1014 1075 1315 1407 1497
270 532 533 558 640 705 991 1054 1140 1164 1295 1609 1741 1985 2374
2326
568 1672
31 335
31 335
62
438 501 534 543 612 658 769 1366 1776 2328
451
204 451 585 1120 1500 2407
558 1984 2142
553
995 2353
528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
533
520 2379
568
1074
243 1210 1216 1396 1504 1805 1849 1889 2140 2337
41 387 1296 1897 2375 2387
2368
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```
sacI (GAGCTC) : 484 2342
balI (GTCGAC) : 2348
bapI (GCTCTTCNNNN) : 15 486 1099
sau3AI (GATC) : 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
2183
sau96I (GNNCC) : 533 534 559 705 769 909 1140 1776 1985 2143 2369
2378
sbfI (CCTGCAGG) : 139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342
scrFI (CCNGG) : 1363 1602 1638 2061 2353 2354
1067
sfanI (GCATC) : 10 520 2379 2400
sfci (CTRYAG) : 534
sfII (GCCCCNNNNNGGCC) : 995 2353
62 2006 2147
42
snabI (TACGTA) : 2336
31
speI (ACTAGT) : 40
2378
sphi (GCATGC) : 1528 1949
484 2342
26 43 149 668
63 443 1259 1322 2349
914 1148 1275 1829 2070
38 331 1329
62
sse8387I (CCTGCAGG) : 175 1788 1915 1981 2220 2361
292 312 315 318 321 508 519 522 567 570 672 1235 1552 1756 2017 2024
4 180 1435 2158
55 410 842 942 1250 1382 1623 1668 1748 1880 2107 2359 2363
tsp45I (GTSAC) :
tsp509I (AATT) :
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[illegible]

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